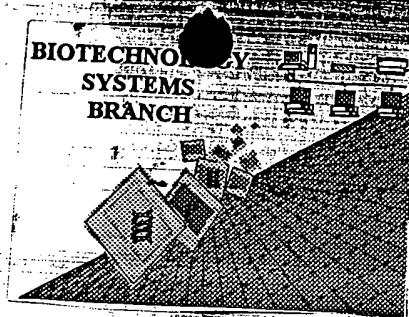


RAW SEQUENCE LISTING **ERROR REPORT**



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/701,001

Source: PR/09

Date Processed by STIC: 1/11/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,

- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

PCT

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/701,001

DATE: 01/11/2001
 TIME: 17:03:22

Input Set: A:\ES.txt
 Output Set: N:\CRF3\01112001\I701001.raw

Does Not Comply
 Corrected Diskette Needed

1 <10> APPLICANT: ASAHIRASEY KOGYO KASUSHIKI KAISHA
 4 <11> ASAHIR MEDICAL CO., LTD.
 6 <12> TITLE OF INVENTION: Separating apparatus of cells and separating method
 8 <13> FILE REFERENCE: ASAHIR-1
 10 <140> CURRENT APPLICATION NUMBER: US/09/701,001
 10 <141> CURRENT FILING DATE: 2000-11-22
 10 <150> PRIOR APPLICATION NUMBER: JP 10/159997
 12 <151> PRIOR FILING DATE: 1998-5-25
 15 <160> NUMBER OF SEQ ID NOS: 18

1998-05-25 ← use this date format

ERRORED SEQUENCES

665 <210> SEQ ID NO: 11
 666 <211> LENGTH: 879
 667 <212> TYPE: DNA
 668 <213> ORGANISM: mouse
 670 <400> SEQUENCE: 41

C--> 671 atg acc atg att acg cca agc ttt gga gcc ttt ttt ttg gag att ttc 48
 672 Met Thr Met Ile Thr Pro Ser Phe Gly Ala Phe Phe Leu Glu Ile Phe
 W--> 673 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95
 674 ggc gtc gaa aac tta tta ttc gca att cct tta gtt gtt cct ttc tat
 675 Asn Val Lys Lys Leu Leu Phe Ala Ile Pro Leu Val Val Pro Phe Tyr
 676 20 25 30
 677 ggc gcc cag cca gcc atg gcc cag atg aag ctg cag cag tct gga cct 144
 678 Ala Ala Gln Pro Ala Met Ala Gln Val Lys Leu Gln Gln Ser Gly Pro
 679 35 40 45
 680 ggc cta gtc cag ccc tca cag agc ctg tcc ttc atc tgc aca gtc tct 192
 681 Gly Leu Val Gln Pro Ser Gln Ser Leu Ser Phe Ile Cys Thr Val Ser
 682 50 55 60
 683 ggt ttc tca tta act agt cat ggt gta cac tgg gtt cgc cag tct cca 240
 684 Gly Phe Ser Leu Thr Ser His Gly Val His Trp Val Arg Gln Ser Pro
 685 65 70 75 80
 686 gga aag ggt ctg gag tgg ctg gga gtc ata tgg ggt gct gga agg aca 288
 687 Gly Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Gly Ala Gly Arg Thr
 688 85 90 95
 689 gac tat aat gca gct ttc ata tcc aga ctg agc atc agc agg gac att 336
 690 Asp Tyr Asn Ala Ala Phe Ile Ser Arg Leu Ser Ile Ser Arg Asp Ile
 691 100 105 110
 692 tcc aag agc caa gtt ttc ttt aag atg aac agt ctg caa gtt gat gac 384
 693 Ser Lys Ser Gln Val Phe Phe Lys Met Asn Ser Leu Gln Val Asp Asp
 694 115 120 125
 695 aca gcc ata tat tac tgt gcc aca aat agg tac gag agc tac ttt gac 432
 696 Thr Ala Ile Tyr Tyr Cys Ala Arg Asn Arg Tyr Glu Ser Tyr Phe Asp
 697 130 135 140
 698 tac tga ggc caa ggg acc acg gtc acc gtc tcc tca ggt gga ggc ggt 480
 699 Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly

see item 4 on
 Error
 Summary
 sheet

```
Input Set : A:\ES.txt
Output Set: N:\CRF3\01112001\1701001.raw
```

[illegible]

Yr Asn Ala Ala Phe Ile Ser
misaligned nos. - see Jess 4 on Enca Summary

sequence of light chain CDR-1
Asn Gly Asn Thr Tyr Leu His

fix nos.

FyI:

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

```
Input Set : A:\ES.txt
Output Set: N:\CRF\01112001\1701001.raw
```

```

L:110 H:1270 C: Current Application Header differs. Replaced Current Application No
L:110 H:1271 C: Current Filing Date differs. Replaced Current Filing Date
L:110 H:110 C: Value Numeric Header Field. Wrong Prior FILING ACTIVITY-REG-00
L:110 H:112 C: (15) String data converted to lower case.
H:112 repeated in sample
L:110 H:112 C: (43) String data converted to lower case.
H:112 repeated in sample
L:111 H:111 C: (43) String data converted to lower case.
H:112 repeated in sample
L:111 H:112 C: (43) String data converted to lower case.
H:112 repeated in sample
L:116 H:280 W: Missing Blank Line separator. <229> field identifier
L:117 H:112 C: (43) String data converted to lower case.
L:127 H:112 C: Missing Blank Line separator. <229> field identifier
L:128 H:112 C: (18) String data converted to lower case.
L:136 H:283 W: Missing Blank Line separator. <229> field identifier
L:139 H:112 C: (43) String data converted to lower case.
L:140 H:112 C: Missing Blank Line separator. <229> field identifier
L:150 H:179 W: Indicator, Feature missing. <221> not found for FFO ID:11
L:150 H:176 W: Mandatory feature missing. <222> not found for SFO ID:11
L:150 H:140 W: (45) "n" or "Xaa" used: Feature required, for SFO ID:14
L:150 H:112 C: (43) String data converted to lower case.
L:161 H:283 W: Missing Blank Line separator. <229> field identifier
L:161 H:282 W: Indicator, Feature missing. <221> not found for SFO ID:15
L:161 H:176 W: Indicator, Feature missing. <222> not found for SFO ID:15
L:161 H:140 C: (45) "n" or "Xaa" used: Feature required, for SFO ID:15
L:161 H:112 C: (43) String data converted to lower case.
L:166 H:283 W: Missing Blank Line separator. <229> field identifier
L:169 H:112 C: (43) String data converted to lower case.
L:176 H:283 W: Missing Blank Line separator. <229> field identifier
L:180 H:112 C: (43) String data converted to lower case.
L:186 H:283 W: Missing Blank Line separator. <229> field identifier
L:186 H:112 C: (48) String data converted to lower case.
L:194 H:283 W: Missing Blank Line separator. <229> field identifier
L:199 H:112 C: (43) String data converted to lower case.
L:196 H:283 W: Missing Blank Line separator. <229> field identifier
L:199 H:112 C: (48) String data converted to lower case.
L:206 H:283 W: Missing Blank Line separator. <229> field identifier
L:206 H:112 C: (48) String data converted to lower case.
L:206 H:283 W: Missing Blank Line separator. <229> field identifier
L:206 H:112 C: (43) String data converted to lower case.
L:206 H:283 W: Missing Blank Line separator. <229> field identifier
L:206 H:112 C: (45) String data converted to lower case.
L:206 H:283 W: Missing Blank Line separator. <229> field identifier
L:210 H:112 C: (48) String data converted to lower case.
L:216 H:283 W: Missing Blank Line separator. <229> field identifier

```

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/701,001

DATE: 01/11/2001

TIME: 17:00:00

Input Set : A:\ES.txt

Output Set: N:\CRF3\01112001\I701001.raw

L:420 M:112 C: (48) String data converted to lower case.
 L:425 M:283 W: Missing Blank Line separator, <220> field identifier
 L:430 M:112 C: (48) String data converted to lower case.
 L:435 M:283 W: Missing Blank Line separator, <220> field identifier
 L:440 M:112 C: (48) String data converted to lower case.
 L:445 M:283 W: Missing Blank Line separator, <220> field identifier
 L:450 M:112 C: (48) String data converted to lower case.
 L:455 M:283 W: Missing Blank Line separator, <220> field identifier
 L:460 M:112 C: (48) String data converted to lower case.
 L:465 M:283 W: Missing Blank Line separator, <220> field identifier
 L:470 M:112 C: (48) String data converted to lower case.
 L:475 M:283 W: Missing Blank Line separator, <220> field identifier
 L:480 M:112 C: (48) String data converted to lower case.
 L:485 M:283 W: Missing Blank Line separator, <220> field identifier
 L:490 M:283 W: Missing Blank Line separator, <220> field identifier
 L:500 M:112 C: (48) String data converted to lower case.
 L:505 M:112 C: (48) String data converted to lower case.
 L:510 M:112 C: (48) String data converted to lower case.
 M:112 Repeated in SeqNo=37
 L:583 M:112 C: (18) String data converted to lower case.
 M:112 Repeated in SeqNo=38
 L:619 M:112 C: (18) String data converted to lower case.
 M:112 Repeated in SeqNo=39
 L:641 M:112 C: (18) String data converted to lower case.
 M:112 Repeated in SeqNo=40
 L:671 M:112 C: (48) String data converted to lower case.
 L:672 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:41
 M:112 Repeated in SeqNo=41
 L:721 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:41
 L:727 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:41
 L:727 M:252 C: No. of Seq. differs, <241-LENGTH:Input:879 Found:909 SEQ:41
 L:735 M:112 C: (18) String data converted to lower case.
 L:747 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:42
 M:112 Repeated in SeqNo=42
 L:788 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:42
 L:791 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:42
 L:794 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:42
 L:800 M:283 W: Missing Blank Line separator, <220> field identifier
 L:810 M:283 W: Missing Blank Line separator, <220> field identifier
 L:815 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:44
 L:821 M:283 W: Missing Blank Line separator, <220> field identifier
 L:831 M:283 W: Missing Blank Line separator, <220> field identifier
 L:836 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:46
 L:842 M:283 W: Missing Blank Line separator, <220> field identifier
 L:852 M:283 W: Missing Blank Line separator, <220> field identifier

PCT

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/701,001
 DATE: 01/11/2001
 TIME: 17:02:22

Input Set : A:\ES.txt
 Output Set: N:\CRF3\01112001\I701001.raw

Does Not Comply
 Corrected Diskette Needed

3 <110> APPLICANT: ASAHIKASEI KOGYO KABUSHIKI KAISHA
 4 ASAHI MEDICAL CO., LTD.
 6 <120> TITLE OF INVENTION: Separating apparatus of cells and separating method
 8 <130> FILE REFERENCE: ASAH-1
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/701,001
 OK 10 <141> CURRENT FILING DATE: 2000-11-22
 10 <150> PRIOR APPLICATION NUMBER: JP 10/159957
 W--> 12 <151> PRIOR FILING DATE: 1998-5-25 1998-05-25 ← use this date format
 15 <160> NUMBER OF SEQ ID NOS: 48

ERRORED SEQUENCES

665 <210> SEQ ID NO: 41
 666 <211> LENGTH: 879 909 shown
 667 <212> TYPE: DNA
 668 <213> ORGANISM: mouse
 670 <400> SEQUENCE: 41
 C--> 671 atg acc atg att acg cca agc ttt gga gcc ttt ttt ttg gag att ttc 48
 672 Met Thr Met Ile Thr Pro Ser Phe Gly Ala Phe Phe Leu Glu Ile Phe
 W--> 673 ~~5~~ 5 ~~10~~ 10 ~~15~~ 15 see item 4 on
 674 aac gtg aaa aaa tta tta ttc gca att cct tta gtt gtt cct ttc tat 96
 675 Asn Val Lys Lys Leu Leu Phe Ala Ile Pro Leu Val Val Pro Phe Tyr
 676 20 25 30
 677 gcg gcc cag ccg gcc atg gcc cag gtg aag ctg cag cag tct gga cct 144
 678 Ala Ala Gln Pro Ala Met Ala Gln Val Lys Leu Gln Gln Ser Gly Pro
 679 35 40 45
 680 ggc cta gtg cag ccc tca cag agc ctg tcc ttc atc tgc aca gtc tct 192
 681 Gly Leu Val Gln Pro Ser Gln Ser Leu Ser Phe Ile Cys Thr Val Ser
 682 50 55 60
 683 ggt ttc tca tta act agt cat ggt gta cac tgg gtt cgc cag tct cca 240
 684 Gly Phe Ser Leu Thr Ser His Gly Val His Trp Val Arg Gln Ser Pro
 685 65 70 75 80
 686 gga aag ggt ctg gag tgg ctg gga gtg ata tgg ggt gct gga agg aca 288
 687 Gly Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Gly Ala Gly Arg Thr
 688 85 90 95
 689 gac tat aat gca gct ttc ata tcc aga ctg agc atc agc agg gac att 336
 690 Asp Tyr Asn Ala Ala Phe Ile Ser Arg Leu Ser Ile Ser Arg Asp Ile
 691 100 105 110
 692 tcc aag agc caa gtt ttc ttt aag atg aac agt ctg caa gtt gat gac 384
 693 Ser Lys Ser Gln Val Phe Phe Lys Met Asn Ser Leu Gln Val Asp Asp
 694 115 120 125
 695 aca gcc ata tat tac tgt gcc aga aat agg tac gag agc tac ttt gac 432
 696 Thr Ala Ile Tyr Tyr Cys Ala Arg Asn Arg Tyr Glu Ser Tyr Phe Asp
 697 130 135 140
 698 tac tgg ggc caa ggg acc acg gtc acc gtc tcc tca ggt gga ggc ggt 480
 699 Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly

see item 4 on
 Error
 Summary
 sheet

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER:

09/90/001

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 Misaligned Amino Acid The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
Numbering between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.
- 7 PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) . Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.
- 8 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(OLD RULES) (2) INFORMATION FOR SEQ ID NO:X:
 (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
 This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
(NEW RULES) <210> sequence id number
 <400> sequence id number
 000
- 10 Use of n's or Xaa's. Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES) Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 Use of <213>Organism Sequence(s) are missing this mandatory field or its response.
(NEW RULES)
- 12 Use of <220>Feature Sequence(s) are missing the <220>Feature and associated headings.
(NEW RULES) Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.